



SEQUENCE LISTING

<110> Schwab, M.
Chen, M.

<120> NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO
GENES AND METHODS BASED THEREON

<130> 10200-003-999

<140> 09/830,972

<141> 2001-09-24

<150> PCT/US99/26160

<151> 1999-11-05

<150> 60/107,446

<151> 1998-11-06

<160> 51

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3741

<212> DNA

<213> Rattus sp.

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<221> CDS

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cggctcggct cggcacgact cggcctgcct ggccccctgcc agtcttgccc aacccccaca      180
accgcccgcg actctgagga gaagcggccc tgcggcggct gtagctgcag catcgtcggc      240
gacccgccag cc atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc      291
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Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu	
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cgc agc ccc gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc	627
Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val	
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Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro	
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Pro Pro Pro Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro	
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Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His	
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Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile	
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Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr	
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Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr	
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Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp	

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cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser 430 435 440 445			1587
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agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca aat Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn 480 485 490			1731
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gat acc tta tca aag gtg act gag gca gca gtg tca aac atg cct gaa Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu 510 515 520 525			1827
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gat att gtt atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly 590 595 600 605	2067
gct tct gta gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca Ala Ser Val Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro 610 615 620	2115
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aaa	aag	gag	aaa	att	tct	ttg	caa	atg	gaa	gag	ttt	aat	act	gca	att	2691	
Lys	Lys	Glu	Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile		
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Tyr	Ser	Asn	Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu		
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Ser	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe		
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ccc	acg	ttt	gtc	agt	gct	aaa	gat	gat	tct	cct	aaa	tta	gcc	aag	gag	2835	
Pro	Thr	Phe	Val	Ser	Ala	Lys	Asp	Asp	Ser	Pro	Lys	Leu	Ala	Lys	Glu		
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Tyr	Thr	Asp	Leu	Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln		
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Phe	Lys	Asn	Ile	Tyr	Pro	Lys	Asp	Glu	Val	His	Val	Ser	Asp	Glu	Phe		
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Ser	Glu	Asn	Arg	Ser	Ser	Val	Ser	Lys	Ala	Ser	Ile	Ser	Pro	Ser	Asn		
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Val	Ser	Ala	Leu	Glu	Pro	Gln	Thr	Glu	Met	Gly	Ser	Ile	Val	Lys	Ser		
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Lys	Ser	Leu	Thr	Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu		
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Lys	Glu	Asp	Arg	Ser	Leu	Ser	Ala	Val	Leu	Ser	Ala	Glu	Leu	Ser	Lys		
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act	tca	gtt	gtt	gac	ctc	ctc	tac	tgg	aga	gac	att	aag	aag	act	gga	3219	
Thr	Ser	Val	Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly		
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gtg	gtg	ttt	ggg	gcc	agc	tta	ttc	ctg	ctg	ctg	tct	ctg	aca	gtg	ttc	3267	
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Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys				
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Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala				
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Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His				
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Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp				
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Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr				
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Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile				
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Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile				
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Asp His Tyr Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala				
	1135	1140	1145	
aaa atc caa gca aaa atc cct gga ttg aag cgc aaa gca gat				3741
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Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp				
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Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly				
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Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala	Ala	Pro	Leu	Leu	Asp	65	70	75	80
Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala	85	90	95	
Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro	100	105	110	
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	115	120	125	
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	130	135	140	
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr	145	150	155	160
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	165	170	175	
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu	180	185	190	
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly	195	200	205	
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	210	215	220	
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu	225	230	235	240
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Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe	260	265	270	
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	275	280	285	
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	290	295	300	
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Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp	405	410	415	
Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro	420	425	430	
Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser	435	440	445	
Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His	450	455	460	
Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala	465	470	475	480
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe	Leu	485	490	495	
Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp	Thr	Leu	500	505	510	
Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr				

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Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr	
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Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	
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Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	
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Val	Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	
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Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	
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Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro	
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Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln	Thr	
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Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg	Leu	Ser	Ala	Ser	Pro	Gln	
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Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser	
	770					775					780					
Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu	
785					790					795					800	
Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile	Tyr	Ser	Asn	
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Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu	Ser	Glu	Thr	
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Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Phe	
		835					840					845				
Val	Ser	Ala	Lys	Asp	Asp	Ser	Pro	Lys	Leu	Ala	Lys	Glu	Tyr	Thr	Asp	
		850				855					860					
Leu	Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	Ala	
865					870					875						

Val	Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe
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Gly	Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val
		995					1000					1005			
Ser	Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser
		1010				1015					1020				
Phe	Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu
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Gly	His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu
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Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Ser
			1060					1065					1070		
Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp
		1075					1080					1085			
Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala
		1090				1095						1100			
Leu	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe
1105					1110					1115					1120
Ser	Ile	Pro	Val	Ile	Tyr	Glu	Arg	His	Gln	Val	Gln	Ile	Asp	His	Tyr
			1125						1130					1135	
Leu	Gly	Leu	Ala	Asn	Lys	Ser	Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln
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 <213> Bos sp.

<400> 3
 Glu Tyr Leu Gly Asp Leu Pro Ala Val Leu Pro Thr Glu
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<210> 4
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 <212> PRT
 <213> Bos sp.

<400> 4
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<220>
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 <222> (2)...(2)
 <223> Xaa = any amino acid

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 1 5 10 15

<210> 6
<211> 9
<212> PRT
<213> Bos sp.

<220>
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<222> 2,5
<223> Xaa = any amino acid

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1 5

<210> 7
<211> 11
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<400> 7
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1 5 10

<210> 8
<211> 16
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<213> Bos sp.

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<213> Bos sp.

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1 5 10

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<400> 10
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1 5 10

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<400> 11
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 Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys
 1 5 10

<210> 14
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<210> 15
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 <213> Rattus sp.

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 1 5 10

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 1 5 10

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 <213> Rattus sp.

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 1 5 10 15

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<400> 18
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<212> PRT
<213> Rattus sp.

<400> 19
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1 5 10

<210> 20
<211> 16
<212> PRT
<213> Rattus sp.

<400> 20
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1 5 10 15

<210> 21
<211> 186
<212> PRT
<213> Homo sapiens

<400> 21
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Val Val Ala Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe
35 40 45
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
50 55 60
His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu
65 70 75 80
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr
85 90 95
Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
100 105 110
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu
115 120 125
Phe Asn Gly Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr
130 135 140
Leu Pro Val Val Tyr Val Lys His Gln Ala Gln Ile Asp Gln Tyr Leu
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 35 40 45
 Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
 50 55 60
 His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu
 65 70 75 80
 Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr
 85 90 95
 Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
 100 105 110
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 115 120 125
 Phe Asn Gly Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr
 130 135 140
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 Gly Leu Val Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala
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 Lys Ile Pro Gly Ala Lys Arg His Ala Glu
 180 185

<210> 23
 <211> 186
 <212> PRT
 <213> Gallus gallus

<400> 23
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 Val Val Ala Tyr Leu Ala Leu Ala Gly Leu Ser Ala Thr Ile Ser Phe
 35 40 45
 Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
 50 55 60
 His Pro Phe Lys Ala Tyr Leu Asp Met Glu Met Asn Leu Ser Gln Asp
 65 70 75 80
 Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr
 85 90 95
 Val Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
 100 105 110
 Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu
 115 120 125
 Phe Asn Gly Leu Thr Leu Leu Ile Met Ala Val Val Ser Met Phe Thr
 130 135 140
 Leu Pro Val Val Tyr Asp Lys Tyr Gln Ala Gln Ile Asp Gln Tyr Leu
 145 150 155 160

Gly	Leu	Val	Arg	Thr	His	Ile	Asn	Thr	Val	Val	Ala	Lys	Ile	Gln	Ala
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Lys	Ile	Pro	Gly	Ala	Lys	Arg	Lys	Ala	Glu						
			180					185							

<210> 24
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 <212> PRT
 <213> Bos sp.

<400> 24

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			20					25					30		
Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser	Phe
		35					40					45			
Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly
	50					55					60				
His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu
65					70					75					80
Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Cys	Thr
			85						90					95	
Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser
			100					105					110		
Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu
		115					120					125			
Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser
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Gly	Leu	Ala	Asn	Lys	Asn	Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala
			165						170					175	
Lys	Ile	Pro	Gly	Leu	Lys	Arg	Lys	Ala	Glu						
			180					185							

<210> 25
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 <212> PRT
 <213> Rattus sp.

<400> 25

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			20					25					30		
Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser	Phe
		35					40					45			
Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly
	50					55					60				
His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu
65					70					75					80
Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Ser	Thr
			85						90					95	
Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser
			100					105					110		
Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu

Asp	Gln	Ile	Leu	Arg	Phe	Tyr	Pro	His	Pro	Lys	Ile	Glu	Ile	Pro	Arg
65					70					75					80
Glu	Glu	Thr	Leu	Tyr	Leu	Ala	Gly	Lys	Ala	Val	Ser	His	Ile	Asn	Leu
			85						90					95	
Ile	Leu	Asn	Arg	Met	Ile	Glu	Leu	Leu	Leu	Val	Glu	Lys	Trp	Glu	Asp
		100					105					110			
Ser	Leu	Lys	Phe	Leu	Val	Leu	Leu	Cys	Gly	Ile	Asn	Leu	Leu	Gly	Asp
	115					120					125				
Cys	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Phe	Gly	Met	Cys	Ile	Cys	Cys
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Leu	Thr	Leu	Leu	Tyr	Leu										
145					150										

<210> 28

<211> 3833

<212> DNA

<213> Bos sp.

<400> 28

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<210> 29

<211> 1178

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

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<223> Xaa = any amino acid

<400> 29

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			20					25					30		
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Asp
		35					40					45			
Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser
	50					55					60				
Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp
65					70					75				80	
Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala
				85					90					95	
Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro
			100					105					110		
Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val
		115					120					125			
Ser	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro
	130					135					140				
Pro	Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr

145					150					155				160
Pro	Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala
				165					170					175
Lys	Arg	Arg	Gly	Ser	Ser	Gly	Ala	Val	Val	Xaa	Xaa	Xaa	Xaa	Lys
			180					185					190	
Met	Asp	Leu	Lys	Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln
		195					200					205		
Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Xaa	Pro	Ser
	210					215					220			
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			245					250						255
Glu	Ala	Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys	Thr	Leu	Leu	Ile
		260					265					270		
Arg	Asp	Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly
	275						280					285		
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	290					295					300			Asn
Pro	Arg	Glu	Glu	Ile	Ile	Val	Lys	Asn	Lys	Asp	Glu	Glu	Glu	Lys
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Val	Ser	Asn	Asn	Ile	Leu	His	Xaa	Gln	Gln	Glu	Leu	Pro	Thr	Ala
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Thr	Lys	Leu	Val	Lys	Glu	Asp	Glu	Val	Val	Ser	Ser	Glu	Lys	Ala
		340					345					350		Lys
Asp	Ser	Phe	Asn	Glu	Lys	Arg	Val	Ala	Val	Glu	Ala	Pro	Met	Arg
	355					360					365			Glu
Glu	Tyr	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Arg	Val	Trp	Glu	Val	Lys
370					375					380				Asp
Ser	Lys	Glu	Asp	Ser	Asp	Met	Leu	Ala	Ala	Gly	Gly	Lys	Ile	Glu
385				390						395				400
Asn	Leu	Glu	Ser	Lys	Val	Asp	Lys	Lys	Cys	Phe	Ala	Asp	Ser	Leu
			405					410						415
Gln	Thr	Asn	His	Glu	Lys	Asp	Ser	Glu	Ser	Ser	Asn	Asp	Asp	Thr
		420						425				430		Ser
Phe	Pro	Ser	Thr	Pro	Glu	Gly	Ile	Lys	Asp	Arg	Ser	Gly	Ala	Tyr
	435					440					445			Ile
Thr	Cys	Ala	Pro	Phe	Asn	Pro	Ala	Ala	Thr	Glu	Ser	Ile	Ala	Thr
	450				455					460				Asn
Ile	Phe	Pro	Leu	Leu	Glu	Asp	Pro	Thr	Ser	Glu	Asn	Xaa	Thr	Asp
465				470					475					Glu
Lys	Lys	Ile	Glu	Glu	Lys	Lys	Ala	Gln	Ile	Val	Thr	Glu	Lys	Asn
			485					490					495	Thr
Ser	Thr	Lys	Thr	Ser	Asn	Pro	Phe	Phe	Val	Ala	Ala	Gln	Asp	Ser
	500						505					510		Glu
Thr	Asp	Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys	Val	Thr	Glu	Glu
	515					520					525			Val
Val	Ala	Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu
	530				535				540					Ala
Cys	Glu	Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys	Ile	Ala	Tyr
545				550					555					Glu
Thr	Lys	Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val	Met	Gln	Glu	Ser
			565					570					575	Leu
Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ser	Glu	Ala
	580						585					590		Thr
Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn
	595						600					605		Ser

Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln	Pro	Ser	Ser	Ser	Pro
610						615					620				
Leu	Glu	Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile	Lys	His	Glu	Pro	Glu
625					630					635					640
Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met	Ser	Val	Ser	Leu	Lys	Val	Ser
				645					650					655	
Gly	Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu
			660					665					670		
Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys
		675					680					685			
Glu	Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Asp	Phe	Ser	Asp	Tyr	Ser
	690				695					700					
Glu	Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	Asp	His	Ser	Glu	Leu	Val
705					710					715					720
Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp
				725					730					735	
Ser	Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	Thr	Val	Met	Leu	Val
			740					745					750		
Lys	Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	Met	Ile	Glu	Tyr	Glu
		755					760					765			
Asn	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Pro	Pro	Glu	Gly	Gly	Lys	Pro	Tyr
	770					775				780					
Leu	Glu	Ser	Phe	Lys	Leu	Ser	Leu	Asp	Asn	Thr	Lys	Asp	Thr	Leu	Leu
785					790					795					800
Pro	Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys	Glu	Lys	Ile	Pro	Leu	Gln
				805					810					815	
Met	Glu	Glu	Leu	Ser	Thr	Ala	Val	Tyr	Ser	Asn	Asp	Asp	Leu	Phe	Ile
			820					825					830		
Ser	Lys	Glu	Ala	Gln	Ile	Arg	Glu	Thr	Glu	Thr	Phe	Ser	Asp	Ser	Ser
	835						840					845			
Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Leu	Ile	Ser	Ser	Lys	Thr
	850					855				860					
Asp	Ser	Phe	Ser	Lys	Leu	Ala	Arg	Glu	Tyr	Thr	Asp	Leu	Glu	Val	Ser
865					870					875					880
His	Lys	Ser	Glu	Ile	Ala	Asn	Ala	Pro	Asp	Gly	Ala	Gly	Ser	Leu	Pro
				885					890					895	
Cys	Thr	Glu	Leu	Pro	His	Asp	Leu	Ser	Leu	Lys	Asn	Ile	Gln	Pro	Lys
			900					905					910		
Val	Glu	Glu	Lys	Ile	Ser	Phe	Ser	Asp	Asp	Phe	Ser	Lys	Asn	Gly	Ser
	915						920					925			
Ala	Thr	Ser	Lys	Val	Leu	Leu	Leu	Pro	Pro	Asp	Val	Ser	Ala	Leu	Gly
	930					935					940				
His	Thr	Gln	Ala	Glu	Ile	Glu	Ser	Ile	Val	Lys	Pro	Lys	Val	Leu	Glu
945					950					955					960
Lys	Glu	Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp	Arg
				965					970					975	
Ser	Pro	Ser	Ala	Ile	Phe	Ser	Ala	Asp	Leu	Gly	Lys	Thr	Ser	Val	Val
			980					985					990		
Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe	Gly
	995						1000					1005			
Ala	Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val	Ser
	1010					1015					1020				
Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser	Phe
1025					1030					1035					1040
Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly
				1045					1050					1055	
His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu

		1060						1065					1070				
Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Cys	Thr		
		1075						1080					1085				
Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser		
		1090						1095					1100				
Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe	Thr	Tyr	Val	Gly	Ala	Leu		
1105						1110					1115				1120		
Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Leu	Ala	Leu	Ile	Ser	Leu	Phe	Ser		
				1125						1130					1135		
Val	Pro	Val	Ile	Tyr	Glu	Arg	His	Gln	Ala	Gln	Ile	Asp	His	Tyr	Leu		
			1140						1145					1150			
Gly	Leu	Ala	Asn	Lys	Asn	Val	Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala		
		1155						1160						1165			
Lys	Ile	Pro	Gly	Leu	Lys	Arg	Lys	Ala	Glu								
	1170						1175										

<210> 30
 <211> 1163
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> VARIANT
 <222> (1)...(1163) at all Xaa position
 <223> Xaa = any amino acid

<400> 30

Met	Glu	Asp	Ile	Asp	Gln	Ser	Ser	Leu	Val	Ser	Ser	Ser	Thr	Asp	Ser		
1				5					10					15			
Pro	Pro	Arg	Pro	Pro	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Thr	Glu	Pro		
			20					25					30				
Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Asp		
		35					40					45					
Glu	Asp	Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly		
	50					55					60						
Leu	Ser	Ala	Ala	Ala	Val	Pro	Pro	Ala	Ala	Ala	Ala	Pro	Leu	Leu	Asp		
65					70					75					80		
Phe	Ser	Ser	Asp	Ser	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala		
				85					90						95		
Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro		
			100					105					110				
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser		
		115				120						125					
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro		
	130					135					140						
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr		
145					150					155					160		
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu		
			165						170					175			
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu		
		180						185						190			
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly		
	195					200						205					
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro		
	210					215					220						
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu		
225						230				235					240		

Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	Thr	
				245					250					255		
Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe	
			260					265					270			
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	
		275					280					285				
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	
	290					295					300					
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	
305					310					315					320	
Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly	
				325					330					335		
Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	
			340					345					350			
Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	
	355						360					365				
Phe	Lys	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	
	370					375					380					
Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp	
385					390					395					400	
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp	
				405					410					415		
Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro	
			420					425					430			
Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser	
	435						440					445				
Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His	
	450					455					460					
Thr	Ser	Glu	Asn	Xaa	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala	
465					470					475					480	
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe	Leu	
				485					490					495		
Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp	Thr	Leu	
			500					505					510			
Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr	
	515						520					525				
Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr	
	530					535					540					
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser	
545					550					555					560	
Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser	
				565					570					575		
Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	
			580					585					590			
Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	
	595						600					605				
Val	Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	
	610					615					620					
Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	
625					630					635					640	
Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	Glu	
				645					650					655		
Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	
			660					665					670			
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro	
	675						680					685				
Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys	Ser	

690		695		700
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu				
705		710		715
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr				
	725		730	735
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser				
	740		745	750
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln				
	755		760	765
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser				
	770		775	780
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu				
785		790		795
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn				
	805		810	815
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr				
	820		825	830
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe				
	835		840	845
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp				
	850		855	860
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala				
865		870		875
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn				
	885		890	895
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn				
	900		905	910
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala				
	915		920	925
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu				
	930		935	940
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp				
945		950		955
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val				
	965		970	975
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe				
	980		985	990
Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val				
	995		1000	1005
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser				
	1010		1015	1020
Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu				
1025		1030		1035
Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu				
	1045		1050	1055
Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser				
	1060		1065	1070
Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp				
	1075		1080	1085
Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala				
	1090		1095	1100
Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe				
1105		1110		1115
Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr				
	1125		1130	1135
Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln				
	1140		1145	1150

Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp
1155 1160

<210> 31
<211> 1568
<212> DNA
<213> Rattus sp.

<400> 31
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gtttctgttg gtatgcataa tttgtaattg ctgctggagg gcagatcgtg gcaagaaatg 120
gacggacaga agaaacattg gaaggacaag gttgttgacc tcctctactg gagagacatt 180
aagaagactg gagtgggtgt tgggtgccagc ttattcctgc tgctgtctct gacagtgttc 240
agcattgtca gtgtaacggc ctacattgcc ttggccctgc tctcgggtgac tatcagcttt 300
aggatatata agggcgtgat ccaggctatc cagaaatcag atgaaggcca cccattcagg 360
gcataatttag aatctgaagt tgctatatca gaggaattgg ttcagaaata cagtaattct 420
gctcttggtc atgtgaacag cacaataaaa gaactgaggc ggcttttctt agttgatgat 480
ttagttgatt ccctgaagtt tgcagtgttg atgtgggtgt ttacttatgt tgggtgccttg 540
ttcaatggtc tgacactact gatttttagct ctgatctcac tcttcagtat tcctgttatt 600
tatgaacggc atcaggtgca gatagatcat tatctaggac ttgcaaacia gagtgttaag 660
gatgccatgg ccaaaatcca agcaaaaatc cctggattga agcgcaaagc agattgaaaa 720
agcccaaac agaagttcat ctttaaaggg gacactcact tgattacggg ggtgggaggt 780
caggggtgag cccttggtgg ccgtgcggtt tcagctcttt attttttagca gtgcactgtt 840
tgaggaaaaa ttacctgtct tgacttcctg tgtttatcat ctttaagtatt gtaagctgct 900
gtgtatggat ctcatgttag tcacacttgt cttccccaat gaggcgcctg gtgaataaag 960
gactcgggga aagctgtgca ttgtatctgc tgcagggtag tctagctgta tgcagagagt 1020
tgtaaagaag gcaaatctgg gggcagggaa aacccttttc acagtgtact gtgtttggtc 1080
agtgtaaaac tgatgcagat ttttctgaaa tgaaatgttt agatgagagc atactactaa 1140
agcagagtgg aaaactctgt ctttatgggtg tgttctaggt gtattgtgaa tttactgtta 1200
tattgccaat ataagtaa atagacctaa tctatatata gtgtttcaca aagcttagat 1260
ctttaacctt gcagctgccc cacagtgcct gacctctgag tcattggtta tgcagtgtag 1320
tcccaagcac ataaactagg aagagaaatg tattttaggt agtgctacct accacctgtt 1380
ttcaagaaaa tatagaactc caacaaaaat atagaatgtc atttcaaaga cttactgtat 1440
gtatagttaa ttttgtcaca gactctgaaa ttctatggac tgaatttcat gcttccaaat 1500
gtttgcagtt atcaaacatt gttatgcaag aaatcataaa atgaagactt ataccattgt 1560
ggtttaag 1568

<210> 32
<211> 199
<212> PRT
<213> Rattus sp.

<400> 32
Met Asp Gly Gln Lys Lys His Trp Lys Asp Lys Val Val Asp Leu Leu
1 5 10 15
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
20 25 30
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
35 40 45
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
50 55 60
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
65 70 75 80
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
85 90 95
Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser Thr Ile Lys Glu

100 105 110
 Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
 115 120 125
 Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
 130 135 140
 Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val
 145 150 155 160
 Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala
 165 170 175
 Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
 180 185 190
 Gly Leu Lys Arg Lys Ala Asp
 195

<210> 33
 <211> 18
 <212> PRT
 <213> Bos sp.

<400> 33
 Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
 1 5 10 15
 Glu Ala

<210> 34
 <211> 13
 <212> DNA
 <213> Homo sapiens

<400> 34
 gccgcccrrcca tgg 13

<210> 35
 <211> 248
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (248) at all n positions
 <223> n=a, c, g or t

<400> 35
 gagccgtcac cacagtaggt ccctcggtc agtcggccca gccctctca gtcctcccca 60
 acccccacaa ccgcccgcgc tcctgagacg cgccccggcg gcggcggc an agctgcagca 120
 tcattctccac cctccagcca tggaagacct ggaccagtct cctctggtct cgtcctcgga 180
 cagcccaccc cggccgcagc ccgcgttcaa gtaccagttc gtgagggagc ccgaggacga 240
 ggaggaag 248

<210> 36
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)... (36) at all n positions
 <223> n=a, c, g or t

<400> 36

gaaaatatgg	acttgaagga	gcagccaggt	aacactat	cggttggtca	agaggatttc	60
ccatctgtcc	tgcttgaaac	tgctgcttct	nttccttctc	tgtctcctct	ctcagccgct	120
tctttcaaag	aacatgaata	ccttggtaat	ttgtcaacag	tattaccac	tgaaggaaca	180
cttcaagaaa	atgtcagtga	agcttctaaa	gaggtctcag	agaaggcaaa	aactctactc	240
atagatagag	atttaacaga	gttttcagaa	ttaggaatac	tcagaaatgg	gatcatcggt	300
cagtgtctct	ccaaaagcag	aatctgccgt	aaatagtagg	caaatcctag	gggaagaaat	360
aattcgtgga	aaaataaag					379

<210> 37
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (281) at all n positions
 <223> n=a, c, g or t

<400> 37

gatagagatt	taacagagtt	ttcagaatta	gaatactcag	aaatgggatc	atcgttcagt	60
gtctctccaa	aagcagaatc	tgccgtaata	gtagcaaatc	ctagggaaga	aataatcggt	120
aaaaataaag	atgaagaaga	gaagttagtt	agtaataaca	tccttcatan	tcaacaagag	180
ttacctacag	ctcttactaa	attggttaaa	gaggatgaag	ttgtgtcttc	agaaaaagca	240
aaagacagtt	ttatgaaaga	gagttgcagt	ggaantcctt	g		281

<210> 38
 <211> 640
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (640) at all n positions
 <223> n=a, c, g or t

<400> 38

ttaaagagga	tgaagtgtg	tcttcagaaa	aagcaaaaaga	cagttttaat	gaaaagagag	60
ttgcagtgga	agctcctatg	agggaggaat	atgcagactt	caaaccattt	gagcgagtat	120
gggaagtga	agatagtaag	gaagatagtg	atatgttggc	tgctggaggt	aaaatcgaga	180
gcaacttgga	aagtaaagtg	gataaaaaat	gttttgcaga	tagccttgag	caaactaatc	240
acgaaaaaga	tagtgagagt	agtaatgatg	atacttcttt	ccccagtacg	ccagaaggta	300
taaaggatcg	ttcaggagca	tatatcacat	gtgctccctt	taaccagca	gcaactgaga	360
gcattgcaac	naacattttt	cctttgttgg	agatcctact	tcagaaaatt	agaccgtgaa	420
aaaaaataga	agaaaaagaag	gccnaatggt	accgagaaga	atactagcac	aaantcaac	480
cctttcttgt	gcagcacagg	ntctgngaca	gatatgtccc	acgnttatta	ccaagtgtg	540
agantcttgc	aacatcctga	ngctgactcc	gattgttccn	gagctttgaa	tggattgtgg	600
ttctggtcaa	gttntttgan	caaattggctt	gtcactcgat			640

<210> 39
 <211> 346
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (346) at all n positions
 <223> n=a, c, g or t

<400> 39
 ctgtgccccg cccaccccc tgggcagatg tccccactg ctaaggctgc tggcttcagg 60
 gagggtttagc ctgcaccgcc gccaccctgc ccctaagtta ttacctctcc agttcctacc 120
 gtactccctg caccgtctca ctgtgtgtnt cgtgtcagta atttatatgg tgttaaaatg 180
 tgtatatttt tgtatgtnac tattttnact agggctgagg ggccctgcgcc cagagctggc 240
 ctcccncaac acctgctgcg cttggttaggt gtggtggcgt tatggcagcc cggctgctgc 300
 ttgatgcca gnttggncctt gggccggtgc tggggggcac agttgt 346

<210> 40
 <211> 325
 <212> DNA
 <213> Homo sapiens

<400> 40
 gtggcaaaaca tgcctgaagg cctgactcca gatttagtac aggaagcatg tgaaagtga 60
 ttgaatgaag ttactggtag aaagattgct tatgaaacaa aatggacttg gttcaaacat 120
 cagaagttat gcaagagtca ctctatcctg cagcacagct ttgcccatca tttgaagagt 180
 cagaagctac tccttcacca gttttgcctg acattgttat ggaagcacca ttgaattctg 240
 cagttcctag tgctgggtgt tccgtgatac agcccagctc atcaccatta gaggcttctt 300
 cagttaatta tgaagcataa acatg 325

<210> 41
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 41
 gcatgtgaaa gtgaattgaa tgaagttact ggtacaaaga ttgcttatga aacaaaaatg 60
 gacttggttc aaacatcaga agttatgcaa gagtcactct atcctgcagc acagctttgc 120
 ccatcatttg aagagtcaga agctactcct tcaccagttt tgcctgacat tgttatggaa 180
 gcaccattga attctgcagt tcctagtgtc ggtgcttccg tgatacagcc cagctcatca 240
 ccattagaag cttcttcagt taattatgaa agcataaaac atgagcctga aaacccccca 300
 ccatatgaag aggccatgag tgtatcacta aaaaaagt 338

<210> 42
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (480) at all n positions
 <223> n=a, c, g or t

<400> 42
 aagactggag tgggtgtttg tgccagccta ttctgtctgc tttcattgac agtattcagc 60
 attgtgagcg taacagccta cattgccttg gccctgctct ctgtgaccat cagcttttagg 120
 atatacaagg gtgtgatcca agctatccag aaatcagatg aaggccaccc attcagggca 180
 tatctggaat ctgaagttgc tataatctgag gagttggttc agaagtacag taattctgct 240
 cttggtcatg tgaactgcac gataaaggaa ctcaggcgcc tcttcttagt tgatgattta 300
 gttgattctc tgaagtttgc agtgttgatg tgggtattta cctatgttgg tgccttgttt 360

aatgggtctga cactactgat ttnggctctc attccactcc tncaagtgtt cctgggtattt 420
 ntgaacggca tcnggcacag ntagatcatt atccaggact tgcaaataagg aatgtaaaga 480

<210> 43
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser
 1 5 10

<210> 44
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 44
 Lys Ile Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly
 1 5 10 15

<210> 45
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 45
 Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn
 1 5 10 15
 Glu Lys Arg

<210> 46
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 46
 Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu
 1 5 10 15
 Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
 20 25 30
 Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro
 35 40 45
 Ser Ser
 50

<210> 47
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate oligonucleotides designed from the bovine NI220
 peptide 1 sequence

<220>

<221> modified base
 <222> (1)... (26) at all n positions
 <223> n=inosine

 <400> 47
 tcngtnggya anacngcngg yaartc 26

 <210> 48
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> degenerate oligonucleotides designed from the bovine NI220
 peptide 1 sequence

 <220>
 <221> modified base
 <222> (1)... (23) at all n positions
 <223> n=inosine

 <400> 48
 tcngtnggna gnacnggyaa ytc 23

 <210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> degenerate oligonucleotides designed from the bovine NI220
 peptide 1 sequence

 <220>
 <221> modified base
 <222> (1)... (25) at all n positions
 <223> n=inosine

 <400> 49
 tcngtnggya anacngcngg agrtc 25

 <210> 50
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> degenerate oligonucleotides designed from the bovine NI220
 peptide 1 sequence

 <220>
 <221> modified base
 <222> (1)... (26) at all n positions
 <223> n=inosine

 <400> 50
 tcngtnggna gnacngcngg nagrtc 26

<210> 51
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220
peptide 2 sequence

<220>
<221> modified_base
<222> (1)... (26) at all n positions
<223> n=inosine

<400> 51
garathgcng anathcarga yggnga